

SEQUENCE LISTING

<110> Ajinomoto Co., Inc.

<120> A new aminopeptidase and the gene encoding the peptidase

<130> Y1J0140

<150> JP 2001-78930

<151> 2001-03-19

<150> JP 2001-293348

<151> 2001-09-26

<160> 15

<170> PatentIn Ver. 2.1

<210> 1

<211> 3383

<212> DNA

<213> Aspergillus nidulans

<400> 1

gggagaagtg tcgcaggatc gagtgtttgt cagtgtgctg gtcacggagc cgagccaggt 60
gcatattcag attgggcctg cagcatctag agtcttgatt gcaaaggagt cggagtaaa 120
tcactattcc gtgcctttcg acggacattc agggccggtg aggattgcga ttgtccgaca 180
tggtagagaa gttaagaccg caacagggcc tgctataacg gaagagtgcg cggacggtaa 240

agtaaattgg aatgcatttg taggatcaag ttaatcgata taaaattgta ctagacacta 300
 aaagcgttgg gataaatggt atctagataa cttgtatgat gtttgcaata tcggggcctg 360
 ttatcgccag gcccggcctc ccagccactg ataagcgtca ctcctcagtt ctccgcatga 420
 ccgcatcttc cttcgctctt ctccaactct cctctctgtc gatgtcctct tcaccatctc 480
 tcttgtttcc atatccttag cctttctatt gcatttttat ttatcttttg aatatggcca 540
 agaaaattct gtctgacatc caccacatg agtctaactt ggcttaccgc cagtatgccc 600
 agctgcctga aaccctccac ctcaactacc agcctcctac tgctactgca acccccgcgc 660
 cacacaccag cccgatccca gaggcaatca accccgacga ttactcgag gcttactgcg 720
 attttatgac tgagcatccc accatttttc acgcagtcga tggcttctct aagcaactcg 780
 aaagcaaggg atacaagtac ctatccgagc gggaattatg gacgccgcag ctcaaacgcg 840
 gaggaaagta ctatacgact cgcaatggaa gctcgttgat tgcgttctct gtcggccccg 900
 agtataagag tgggaatggc ctgctatca tcgccggcca cattgatgcc ctacggcga 960
 agctcaagcc cgtctcaaaa ctccccata aagctggata cattcagatg ggagttgctc 1020
 cttatgccgg cggctctgggc aagacatggt gggaccgtga tttgtctatc ggcggaagg 1080
 ttctcgttcg taacgctagc accggcaagg ttgaatccaa gctagtcaag ttgaactggc 1140
 cgattgctcg catcccaacg ctagccgaac actttggcgc tccttcgcag gggccattca 1200
 acaaggaaac acagatggta cctatcattg gagtcgacaa ctctgatctt ttccagtcta 1260
 ccactccagc ggcagacgag ggcatcgaac ccggcacctt tgcctctacg cagcccccaa 1320
 aactcatcaa agtgatctcc aaggaacttg gaatcacaaa ctacagcagc attctcagct 1380
 gggagctaga actttatgac agccagcctg cacgtatcgg cggatttgac aaggatttta 1440
 tcttcgccgg ccgcatcgat gacaagctct gctgctacgc cgcacaggaa gccctcatgg 1500
 ctacctcga ccacacctct cctcttcca tcaagatggt cggttacttt gatgatgagg 1560
 aaattggtag cttgctccgt cagggtgccc gtcceaactt catgtctagc gtcacgaac 1620
 gcattgcaca atcctttgca acatcatatg gaccgatct cttgccccaa accgttgcaa 1680
 agagcttctt tatctcttct gatgtcatcc acgtgtcaa tcccaacttc ttgaatgtct 1740
 atctcgagaa ccacgcgcct cgtctcaatg tcggcgtctc cgtctccgca gactcaaacg 1800
 gccacatgac taccgacagt gtcagctacg gttcatcaa gcgcgttgct gaaaagtgcg 1860
 gctctcagct gcaggtcttt caaatccgaa atgactcccc aagcggcgga accattgggc 1920
 ccatgaccag ctgcgcgatt ggaatgaggg ccattgatgt cggtatccca cagttgagca 1980

tgcatacatgcat tgcgccacc acaggagatc gcgatcctgg gctgggtgtc aagctgttta 2040
 aggggttctt tgattacttt gaagaggtgg atcgtgagtt ttctgatttt taggttgtga 2100
 ctcttgtttt ctgtcgaggg gtgtgtgtgc gctgcttggc cgtgtctagt ttggtttgca 2160
 tgattttggt gctaggggtt aagtgttgg gcattaagaa cctcatttag aatggtgact 2220
 tctttgtata cggggttcgg agtccgtcta tagaggcatg tgtaaggata aaaatcgaat 2280
 cctacataat tccaggctat gcacttgaac agacaacatc tagattctag gcacgtcaaa 2340
 ccatacaata tattaagagg cttccgtcta ttgatgtct caccggcac gaatctcaac 2400
 agtaagcccc gtagtctact ccgtacttct tgcctgccga aggagaggat ggagatgagg 2460
 gtgacgaatg cgttgttttc accagtgtccc caatgacagt tgcattatcc tcaatttaat 2520
 cagccccgtc tcttccagt tccacccag ctttggagc agtccgggca atgtctctctg 2580
 cgacacttac tgtcatgatc cccctacata aacacacggc ttgcagccc cagccccagc 2640
 cccattcagg gccaaaagct ctagactgat ccgcatccca ctcacaactc ccatgttcca 2700
 aatcattgat gtgcgttggt attgtagtag aaatgcccac tccccaatg ctccagaaaa 2760
 ctggcgggccg gggttcttgc ccaactgtaa gcgctaggct ccgagataat ctcttagact 2820
 tggatttcga tctggatctg gggttgctgt gcgatgagag gagttgtgga atcatagggg 2880
 aaagcagggg ccgcagagtc ggtaggcagg cgcagactat gccgacgttg cattccactg 2940
 cggaccaggt tgcggcaccg acgttgtcat ctgcttgtcg ttagtagggg ttttttggg 3000
 ttgatggagg gacgtacagg ttgggtccga agagtcagcg attcttttta gggacatcaa 3060
 acggcaaagt cttgttatgc agacgctaga attactcagg attagcagat gcacacaccg 3120
 accatggaac agaaaacgta caaaccccc accgcaaaa ttgcaataag agcaactctc 3180
 tgcttccttg gcaaatcaag actatacaag gcaggtatag ggataactag gatagcaagg 3240
 tccgtcgcaa tatgcattga agcattggag aaccacagag ctttcgaact gagacatgat 3300
 cccgggattg ttgggtccca gaaacgtgct actggtatgc agttcaagaa cccgctaagc 3360
 acagcccatg tgccgattga cga 3383

<210> 2

<211> 1916

<212> DNA

<213> Aspergillus nidulans

<220>

<221> CDS

<222> (72)..(1628)

<400> 2

tgctctcttc accatctctc ttgtttccat atccttagcc tttctattgc atttttattt 60

atcttttgaa t atg gcc aag aaa att ctg tct gac atc cac cac cat gag 110

Met Ala Lys Lys Ile Leu Ser Asp Ile His His His Glu

1

5

10

tct aac ttg gct tac cgc cag tat gcc cag ctg cct gaa acc ctc cac 158

Ser Asn Leu Ala Tyr Arg Gln Tyr Ala Gln Leu Pro Glu Thr Leu His

15

20

25

ctc aac tac cag cct cct act gct act gca acc ccc gcc gca cac acc 206

Leu Asn Tyr Gln Pro Pro Thr Ala Thr Ala Thr Pro Ala Ala His Thr

30

35

40

45

agc ccg atc cca gag gca atc aac ccc gac gat tac tcg cag gct tac 254

Ser Pro Ile Pro Glu Ala Ile Asn Pro Asp Asp Tyr Ser Gln Ala Tyr

50

55

60

tgc gat ttt atg act gag cat ccc acc att ttt cac gca gtc gat ggc 302

Cys Asp Phe Met Thr Glu His Pro Thr Ile Phe His Ala Val Asp Gly

65

70

75

ttc tct aag caa ctc gaa agc aag gga tac aag tac cta tcc gag cgg 350
Phe Ser Lys Gln Leu Glu Ser Lys Gly Tyr Lys Tyr Leu Ser Glu Arg

80

85

90

gaa tta tgg acg ccg cag ctc aaa cgc gga gga aag tac tat acg act 398
Glu Leu Trp Thr Pro Gln Leu Lys Arg Gly Gly Lys Tyr Tyr Thr Thr

95

100

105

cgc aat gga agc tcg ttg att gcg ttc tct gtc ggc ccc gag tat aag 446
Arg Asn Gly Ser Ser Leu Ile Ala Phe Ser Val Gly Pro Glu Tyr Lys
110 115 120 125

agt ggg aat ggc ctc gct atc atc gcc ggc cac att gat gcc ctc acg 494
Ser Gly Asn Gly Leu Ala Ile Ile Ala Gly His Ile Asp Ala Leu Thr
130 135 140

gcg aag ctc aag ccc gtc tca aaa ctt ccc aat aaa gct gga tac att 542
Ala Lys Leu Lys Pro Val Ser Lys Leu Pro Asn Lys Ala Gly Tyr Ile
145 150 155

cag atg gga gtt gct cct tat gcc ggc ggt ctg ggc aag aca tgg tgg 590
Gln Met Gly Val Ala Pro Tyr Ala Gly Gly Leu Gly Lys Thr Trp Trp
160 165 170

gac cgt gat ttg tct atc ggc ggg aag gtt ctc gtt cgt aac gct agc 638
Asp Arg Asp Leu Ser Ile Gly Gly Lys Val Leu Val Arg Asn Ala Ser
175 180 185

acc ggc aag gtt gaa tcc aag cta gtc aag ttg aac tgg ccg att gct 686

Thr Gly Lys Val Glu Ser Lys Leu Val Lys Leu Asn Trp Pro Ile Ala	
190	205
cgc atc cca acg cta gcc gaa cac ttt ggc gct cct tcg cag ggg cca	734
Arg Ile Pro Thr Leu Ala Glu His Phe Gly Ala Pro Ser Gln Gly Pro	
210	220
ttc aac aag gaa aca cag atg gta cct atc att gga gtc gac aac tct	782
Phe Asn Lys Glu Thr Gln Met Val Pro Ile Ile Gly Val Asp Asn Ser	
225	235
gat ctt ttc cag tct acc act cca gcg gca gac gag ggc atc gaa ccc	830
Asp Leu Phe Gln Ser Thr Thr Pro Ala Ala Asp Glu Gly Ile Glu Pro	
240	250
ggc acc ttt gcc tct acg cag ccc cca aaa ctc atc aaa gtg atc tcc	878
Gly Thr Phe Ala Ser Thr Gln Pro Pro Lys Leu Ile Lys Val Ile Ser	
255	265
aag gaa ctt gga atc aca aac tac agc agc att ctc agc tgg gag cta	926
Lys Glu Leu Gly Ile Thr Asn Tyr Ser Ser Ile Leu Ser Trp Glu Leu	
270	285
gaa ctt tat gac agc cag cct gca cgt atc ggc ggt att gac aag gat	974
Glu Leu Tyr Asp Ser Gln Pro Ala Arg Ile Gly Gly Ile Asp Lys Asp	
290	300
ttt atc ttc gcc ggc cgc atc gat gac aag ctc tgc tgc tac gcc gca	1022
Phe Ile Phe Ala Gly Arg Ile Asp Asp Lys Leu Cys Cys Tyr Ala Ala	

305	310	315	
cag gaa gcc ctc atg gct acc tcc gac cac acc tct ccc tct tcc atc			1070
Gln Glu Ala Leu Met Ala Thr Ser Asp His Thr Ser Pro Ser Ser Ile			
320	325	330	
aag atg gtc ggt tac ttt gat gat gag gaa att ggt agc ttg ctc cgt			1118
Lys Met Val Gly Tyr Phe Asp Asp Glu Glu Ile Gly Ser Leu Leu Arg			
335	340	345	
cag ggt gcc cgc tcc aac ttc atg tct agc gtc atc gaa cgc att gca			1166
Gln Gly Ala Arg Ser Asn Phe Met Ser Ser Val Ile Glu Arg Ile Ala			
350	355	360	365
caa tcc ttt gca aca tca tat gga ccc gat ctc ctt gcc caa acc gtt			1214
Gln Ser Phe Ala Thr Ser Tyr Gly Pro Asp Leu Leu Ala Gln Thr Val			
370	375	380	
gca aag agc ttc ctt atc tct tct gat gtc atc cac gct gtc aat ccc			1262
Ala Lys Ser Phe Leu Ile Ser Ser Asp Val Ile His Ala Val Asn Pro			
385	390	395	
aac ttc ttg aat gtc tat ctc gag aac cac gcg cct cgt ctc aat gtc			1310
Asn Phe Leu Asn Val Tyr Leu Glu Asn His Ala Pro Arg Leu Asn Val			
400	405	410	
ggc gtc tcc gtc tcc gca gac tca aac ggc cac atg act acc gac agt			1358
Gly Val Ser Val Ser Ala Asp Ser Asn Gly His Met Thr Thr Asp Ser			
415	420	425	

gtc agc tac ggc ttc atc aag cgc gtt gct gaa aag tgc ggc tct cag 1406
 Val Ser Tyr Gly Phe Ile Lys Arg Val Ala Glu Lys Cys Gly Ser Gln
 430 435 440 445

ctg cag gtc ttt caa atc cga aat gac tcc cga agc ggc gga acc att 1454
 Leu Gln Val Phe Gln Ile Arg Asn Asp Ser Arg Ser Gly Gly Thr Ile
 450 455 460

ggg ccc atg acc agc tcg cgg att gga atg agg gcc att gat gtc ggt 1502
 Gly Pro Met Thr Ser Ser Arg Ile Gly Met Arg Ala Ile Asp Val Gly
 465 470 475

atc cca cag ttg agc atg cat agc att cgc gcc acc aca ggg agt cgc 1550
 Ile Pro Gln Leu Ser Met His Ser Ile Arg Ala Thr Thr Gly Ser Arg
 480 485 490

gat cct ggg ctg ggt gtc aag ctg ttt aag ggg ttc ttt gat tac ttt 1598
 Asp Pro Gly Leu Gly Val Lys Leu Phe Lys Gly Phe Phe Asp Tyr Phe
 495 500 505

gaa gag gtg gat cgt gag ttt tct gat ttt taggttgtga ctcttgtttt 1648
 Glu Glu Val Asp Arg Glu Phe Ser Asp Phe
 510 515

ctgtcgaggg gtgctgtcgc gctgcttggc cgtgtctagt ttggtttgca tgattttggt 1708

gctagggttg aagtgcttgg gcattaagaa cctcatttag aatggtgact tctttgtata 1768

cggggttcgg agtccgtcta tagaggcatg tgtaaggata aaaatcgaat cctacataat 1828

tccaggctat gcacttgaac agacaacatc tagattctag gcacgtcaaa ccatacaata 1888

tattaagagg cttccgtcta tttgatgc 1916

<210> 3

<211> 519

<212> PRT

<213> Aspergillus nidulans

<400> 3

Met Ala Lys Lys Ile Leu Ser Asp Ile His His His Glu Ser Asn Leu

1 5 10 15

Ala Tyr Arg Gln Tyr Ala Gln Leu Pro Glu Thr Leu His Leu Asn Tyr

20 25 30

Gln Pro Pro Thr Ala Thr Ala Thr Pro Ala Ala His Thr Ser Pro Ile

35 40 45

Pro Glu Ala Ile Asn Pro Asp Asp Tyr Ser Gln Ala Tyr Cys Asp Phe

50 55 60

Met Thr Glu His Pro Thr Ile Phe His Ala Val Asp Gly Phe Ser Lys

65 70 75 80

Gln Leu Glu Ser Lys Gly Tyr Lys Tyr Leu Ser Glu Arg Glu Leu Trp

	85	90	95
Thr Pro Gln Leu Lys Arg Gly Gly Lys Tyr Tyr Thr Thr Arg Asn Gly			
	100	105	110
Ser Ser Leu Ile Ala Phe Ser Val Gly Pro Glu Tyr Lys Ser Gly Asn			
	115	120	125
Gly Leu Ala Ile Ile Ala Gly His Ile Asp Ala Leu Thr Ala Lys Leu			
	130	135	140
Lys Pro Val Ser Lys Leu Pro Asn Lys Ala Gly Tyr Ile Gln Met Gly			
145	150	155	160
Val Ala Pro Tyr Ala Gly Gly Leu Gly Lys Thr Trp Trp Asp Arg Asp			
	165	170	175
Leu Ser Ile Gly Gly Lys Val Leu Val Arg Asn Ala Ser Thr Gly Lys			
	180	185	190
Val Glu Ser Lys Leu Val Lys Leu Asn Trp Pro Ile Ala Arg Ile Pro			
	195	200	205
Thr Leu Ala Glu His Phe Gly Ala Pro Ser Gln Gly Pro Phe Asn Lys			
	210	215	220
Glu Thr Gln Met Val Pro Ile Ile Gly Val Asp Asn Ser Asp Leu Phe			
225	230	235	240

Gln Ser Thr Thr Pro Ala Ala Asp Glu Gly Ile Glu Pro Gly Thr Phe
245 250 255

Ala Ser Thr Gln Pro Pro Lys Leu Ile Lys Val Ile Ser Lys Glu Leu
260 265 270

Gly Ile Thr Asn Tyr Ser Ser Ile Leu Ser Trp Glu Leu Glu Leu Tyr
275 280 285

Asp Ser Gln Pro Ala Arg Ile Gly Gly Ile Asp Lys Asp Phe Ile Phe
290 295 300

Ala Gly Arg Ile Asp Asp Lys Leu Cys Cys Tyr Ala Ala Gln Glu Ala
305 310 315 320

Leu Met Ala Thr Ser Asp His Thr Ser Pro Ser Ser Ile Lys Met Val
325 330 335

Gly Tyr Phe Asp Asp Glu Glu Ile Gly Ser Leu Leu Arg Gln Gly Ala
340 345 350

Arg Ser Asn Phe Met Ser Ser Val Ile Glu Arg Ile Ala Gln Ser Phe
355 360 365

Ala Thr Ser Tyr Gly Pro Asp Leu Leu Ala Gln Thr Val Ala Lys Ser
370 375 380

Phe Leu Ile Ser Ser Asp Val Ile His Ala Val Asn Pro Asn Phe Leu
385 390 395 400

Asn Val Tyr Leu Glu Asn His Ala Pro Arg Leu Asn Val Gly Val Ser
405 410 415

Val Ser Ala Asp Ser Asn Gly His Met Thr Thr Asp Ser Val Ser Tyr
420 425 430

Gly Phe Ile Lys Arg Val Ala Glu Lys Cys Gly Ser Gln Leu Gln Val
435 440 445

Phe Gln Ile Arg Asn Asp Ser Arg Ser Gly Gly Thr Ile Gly Pro Met
450 455 460

Thr Ser Ser Arg Ile Gly Met Arg Ala Ile Asp Val Gly Ile Pro Gln
465 470 475 480

Leu Ser Met His Ser Ile Arg Ala Thr Thr Gly Ser Arg Asp Pro Gly
485 490 495

Leu Gly Val Lys Leu Phe Lys Gly Phe Phe Asp Tyr Phe Glu Glu Val
500 505 510

Asp Arg Glu Phe Ser Asp Phe
515

<210> 4

<211> 1679

<212> DNA

<213> *Aspergillus oryzae*

<220>

<221> CDS

<222> (73)..(1602)

<400> 4

caggcttaaa ccgcattccg acaagatata tagcctttaa actaagaaat tttccaactc 60

ctagccttcg ac atg acc aaa agg agt gtc ctt gat ctc cgt gat tct gcc 111

Met Thr Lys Arg Ser Val Leu Asp Leu Arg Asp Ser Ala

1

5

10

atg gct tat cgc ctg tcg gcc cag ctt cct gag ccc tcc cca gcc acc 159

Met Ala Tyr Arg Leu Ser Ala Gln Leu Pro Glu Pro Ser Pro Ala Thr

15

20

25

att gca acc cca gtg gcg agg agt ggc ccc ttc gcc ccg gaa gat tac 207

Ile Ala Thr Pro Val Ala Arg Ser Gly Pro Phe Ala Pro Glu Asp Tyr

30

35

40

45

acg aaa cca tac tgc gaa ttc atg aca gca aac ccc aca atc ttt cac 255

Thr Lys Pro Tyr Cys Glu Phe Met Thr Ala Asn Pro Thr Ile Phe His

50

55

60

gcc gtt gat ggt ttc acc agg cag ctc gaa agc cag gga tac aag cgc 303

Ala Val Asp Gly Phe Thr Arg Gln Leu Glu Ser Gln Gly Tyr Lys Arg

65

70

75

ctt ccc gag cgc gag acg tgg aac tcc aag tta gag aag ggt ggg aag	351
Leu Pro Glu Arg Glu Thr Trp Asn Ser Lys Leu Glu Lys Gly Gly Lys	
80 85 90	
tac tac gtc act cgg aat ggt agt gct ttc atc tca ttc tca att gga	399
Tyr Tyr Val Thr Arg Asn Gly Ser Ala Phe Ile Ser Phe Ser Ile Gly	
95 100 105	
aga gat tat aaa agt ggc aat gga atg gcc att gtt gca ggt cat atc	447
Arg Asp Tyr Lys Ser Gly Asn Gly Met Ala Ile Val Ala Gly His Ile	
110 115 120 125	
gat gca ctc acc gcc aaa ttg aag ccc gtg tcc aag ctg ccc aac aag	495
Asp Ala Leu Thr Ala Lys Leu Lys Pro Val Ser Lys Leu Pro Asn Lys	
130 135 140	
gct ggc ttt tcc cag ctc gga gtt gcg ccc tac gca ggc gct ctg agt	543
Ala Gly Phe Ser Gln Leu Gly Val Ala Pro Tyr Ala Gly Ala Leu Ser	
145 150 155	
gac aca tgg tgg gac cgc gat ctc tca ata ggt ggc cgt gtt ctg gtc	591
Asp Thr Trp Trp Asp Arg Asp Leu Ser Ile Gly Gly Arg Val Leu Val	
160 165 170	
caa gac tcc aac acc ggg aaa gtc gag tcc aaa tta gtc aaa ttg gac	639
Gln Asp Ser Asn Thr Gly Lys Val Glu Ser Lys Leu Val Lys Leu Asp	
175 180 185	

tgg ccc att gct cgg atc cca acc ctg gca cct cat ttc ggg gct ccc 687
Trp Pro Ile Ala Arg Ile Pro Thr Leu Ala Pro His Phe Gly Ala Pro
190 195 200 205

tcg caa ggc ccc ttc aac aaa gag act cag atg gtg cct ata att ggc 735
Ser Gln Gly Pro Phe Asn Lys Glu Thr Gln Met Val Pro Ile Ile Gly
210 215 220

ggt gat aac tcc gat ctt ttc cag cag caa gcc cca tcc aag ata gat 783
Val Asp Asn Ser Asp Leu Phe Gln Gln Gln Ala Pro Ser Lys Ile Asp
225 230 235

caa gac aac ggg atc aaa cct ggt aca ttt gca gcc acg caa ccg gaa 831
Gln Asp Asn Gly Ile Lys Pro Gly Thr Phe Ala Ala Thr Gln Pro Glu
240 245 250

aag ctt gtc aaa gtc ata tcc aag gag ctt ggt atc aca gac tac agc 879
Lys Leu Val Lys Val Ile Ser Lys Glu Leu Gly Ile Thr Asp Tyr Ser
255 260 265

tcg att ata agc tgg gag ctg gag ctg tat gac agt caa cca gca caa 927
Ser Ile Ile Ser Trp Glu Leu Glu Leu Tyr Asp Ser Gln Pro Ala Gln
270 275 280 285

gtt ggt ggc ctg gac aag gac ctg att ttt gct ggt cgc att gac gat 975
Val Gly Gly Leu Asp Lys Asp Leu Ile Phe Ala Gly Arg Ile Asp Asp
290 295 300

aag ctc tgc tgc tat gcc gct cag gaa gct ctg ctt gcc tca tcc gac 1023

Lys Leu Cys Cys Tyr Ala Ala Gln Glu Ala Leu Leu Ala Ser Ser Asp	
305	310 315
agt act tca act agc tct atc aag atg gtc ggt atg ttt gat gac gag	1071
Ser Thr Ser Thr Ser Ser Ile Lys Met Val Gly Met Phe Asp Asp Glu	
320	325 330
gaa att gga agc ctg ctt cgc cag gga gct cga tcc aac ttc atg agc	1119
Glu Ile Gly Ser Leu Leu Arg Gln Gly Ala Arg Ser Asn Phe Met Ser	
335	340 345
agt gtc ata gag cgt att acg gaa gcc ttc tca ccc aat tac ggt cct	1167
Ser Val Ile Glu Arg Ile Thr Glu Ala Phe Ser Pro Asn Tyr Gly Pro	
350	355 360 365
aac gtg ctg tct caa act gtg gcg aac agc ttc ttc gtg tct tcg gac	1215
Asn Val Leu Ser Gln Thr Val Ala Asn Ser Phe Phe Val Ser Ser Asp	
370	375 380
gtc atc cat gcg gtc aat ccg aac ttc ctt ggt gtc tat ctt gag aac	1263
Val Ile His Ala Val Asn Pro Asn Phe Leu Gly Val Tyr Leu Glu Asn	
385	390 395
cat gct ccc cgt ctg aac gtc ggt gtg gcc gtc tcg gct gac tct aac	1311
His Ala Pro Arg Leu Asn Val Gly Val Ala Val Ser Ala Asp Ser Asn	
400	405 410
ggc cat atg aca aca gac agt gtg agc tac gga ttc atc aag cgt gtc	1359
Gly His Met Thr Thr Asp Ser Val Ser Tyr Gly Phe Ile Lys Arg Val	

415	420	425	
gct gat cga tgt ggc tcg acc ttg cag gtc ttc cag att cgt aat gac			1407
Ala Asp Arg Cys Gly Ser Thr Leu Gln Val Phe Gln Ile Arg Asn Asp			
430	435	440	445
tcc cgt agt ggc ggg act att gga ccc atg acc agt tct cgc att ggc			1455
Ser Arg Ser Gly Gly Thr Ile Gly Pro Met Thr Ser Ser Arg Ile Gly			
	450	455	460
atg agg gcc att gac gtg ggg atc ccg cag ttg agt atg cac agt atc			1503
Met Arg Ala Ile Asp Val Gly Ile Pro Gln Leu Ser Met His Ser Ile			
	465	470	475
cgt gcg act acc ggt agt ttg gat ccg gga ttg ggt gtg aag ctg ttc			1551
Arg Ala Thr Thr Gly Ser Leu Asp Pro Gly Leu Gly Val Lys Leu Phe			
	480	485	490
aag ggc ttt ttc gac tat ttc gag gag gtg gac aag gaa ttt gca gat			1599
Lys Gly Phe Phe Asp Tyr Phe Glu Glu Val Asp Lys Glu Phe Ala Asp			
	495	500	505
ttc tgatgcgctc ctctggaata ctaggaaatg tttccatcga taagtatgca			1652
Phe			
510			
ctatctggga ttccgatgtt ggatctg			1679

<210> 5

<211> 510

<212> PRT

<213> Aspergillus oryzae

<400> 5

Met Thr Lys Arg Ser Val Leu Asp Leu Arg Asp Ser Ala Met Ala Tyr

1 5 10 15

Arg Leu Ser Ala Gln Leu Pro Glu Pro Ser Pro Ala Thr Ile Ala Thr

20 25 30

Pro Val Ala Arg Ser Gly Pro Phe Ala Pro Glu Asp Tyr Thr Lys Pro

35 40 45

Tyr Cys Glu Phe Met Thr Ala Asn Pro Thr Ile Phe His Ala Val Asp

50 55 60

Gly Phe Thr Arg Gln Leu Glu Ser Gln Gly Tyr Lys Arg Leu Pro Glu

65 70 75 80

Arg Glu Thr Trp Asn Ser Lys Leu Glu Lys Gly Gly Lys Tyr Tyr Val

85 90 95

Thr Arg Asn Gly Ser Ala Phe Ile Ser Phe Ser Ile Gly Arg Asp Tyr

100 105 110

Lys Ser Gly Asn Gly Met Ala Ile Val Ala Gly His Ile Asp Ala Leu

115 120 125

Thr Ala Lys Leu Lys Pro Val Ser Lys Leu Pro Asn Lys Ala Gly Phe
130 135 140

Ser Gln Leu Gly Val Ala Pro Tyr Ala Gly Ala Leu Ser Asp Thr Trp
145 150 155 160

Trp Asp Arg Asp Leu Ser Ile Gly Gly Arg Val Leu Val Gln Asp Ser
165 170 175

Asn Thr Gly Lys Val Glu Ser Lys Leu Val Lys Leu Asp Trp Pro Ile
180 185 190

Ala Arg Ile Pro Thr Leu Ala Pro His Phe Gly Ala Pro Ser Gln Gly
195 200 205

Pro Phe Asn Lys Glu Thr Gln Met Val Pro Ile Ile Gly Val Asp Asn
210 215 220

Ser Asp Leu Phe Gln Gln Gln Ala Pro Ser Lys Ile Asp Gln Asp Asn
225 230 235 240

Gly Ile Lys Pro Gly Thr Phe Ala Ala Thr Gln Pro Glu Lys Leu Val
245 250 255

Lys Val Ile Ser Lys Glu Leu Gly Ile Thr Asp Tyr Ser Ser Ile Ile
260 265 270

Ser Trp Glu Leu Glu Leu Tyr Asp Ser Gln Pro Ala Gln Val Gly Gly

275	280	285
Leu Asp Lys Asp Leu Ile Phe Ala Gly Arg Ile Asp Asp Lys Leu Cys		
290	295	300
Cys Tyr Ala Ala Gln Glu Ala Leu Leu Ala Ser Ser Asp Ser Thr Ser		
305	310	315
Thr Ser Ser Ile Lys Met Val Gly Met Phe Asp Asp Glu Glu Ile Gly		
	325	330
		335
Ser Leu Leu Arg Gln Gly Ala Arg Ser Asn Phe Met Ser Ser Val Ile		
	340	345
		350
Glu Arg Ile Thr Glu Ala Phe Ser Pro Asn Tyr Gly Pro Asn Val Leu		
	355	360
		365
Ser Gln Thr Val Ala Asn Ser Phe Phe Val Ser Ser Asp Val Ile His		
	370	375
		380
Ala Val Asn Pro Asn Phe Leu Gly Val Tyr Leu Glu Asn His Ala Pro		
385	390	395
		400
Arg Leu Asn Val Gly Val Ala Val Ser Ala Asp Ser Asn Gly His Met		
	405	410
		415
Thr Thr Asp Ser Val Ser Tyr Gly Phe Ile Lys Arg Val Ala Asp Arg		
	420	425
		430

Cys Gly Ser Thr Leu Gln Val Phe Gln Ile Arg Asn Asp Ser Arg Ser
435 440 445

Gly Gly Thr Ile Gly Pro Met Thr Ser Ser Arg Ile Gly Met Arg Ala
450 455 460

Ile Asp Val Gly Ile Pro Gln Leu Ser Met His Ser Ile Arg Ala Thr
465 470 475 480

Thr Gly Ser Leu Asp Pro Gly Leu Gly Val Lys Leu Phe Lys Gly Phe
485 490 495

Phe Asp Tyr Phe Glu Glu Val Asp Lys Glu Phe Ala Asp Phe
500 505 510

<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 6

ctcaaacggc cacatgacta c

21

<210> 7

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 7

gtctgttcaa gtgcatagcc tg

22

<210> 8

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 8

caccaccatg agtctaactt gg

22

<210> 9

<211> 22

<212> DNA

s <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 9

gtctgttcaa gtgcatagcc tg

22

<210> 10

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 10

cgtggtacca tggctctagag t

21

<210> 11

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 11

aatcgagta agcctgcgag

20

<210> 12

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 12

cgtggtacca tggcttagag t

21

<210> 13

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 13

catgggccca atggttcgc

20

<210> 14

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 14

ccagattcgt aatgactccc g

21

<210> 15

<211> 32

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:PCR primer

<400> 15

ctactactac taggccacgc gtcgactagt ac

32